

## BLAST

# Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

### Protein Sequence (8 letters)

residues 73-80 of SEQ ID NO: 12

Results for:  ▼

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

#### Query ID

|cl|27776

|cl|27776

#### Description

None

#### Molecule type

amino acid

#### Query Length

8

#### Database Name

nr

#### Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

#### Program

BLASTP 2.2.22+ [Citation](#)

#### Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Multiple alignment](#) [NEW](#)

## Search Parameters

Program	blastp
Word size	2
Expect value	200000
Hitlist size	100
Gapcosts	9,1
Matrix	PAM30
Threshold	11
Filter string	F
Genetic Code	1
Window Size	40

## Database

Posted date	Jan 3, 2010 5:44 PM
Number of letters	3,505,793,397
Number of sequences	10,274,250
Entrez query	none

## Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.368907	0.294
K	0.286243	0.11
H	1.92795	0.61

## Results Statistics

Length adjustment	0
Effective length of query	8
Effective length of database	3505793397
Effective search space	28046347176
Effective search space used	28046347176

[Graphic Summary](#)

[Show Conserved Domains](#)

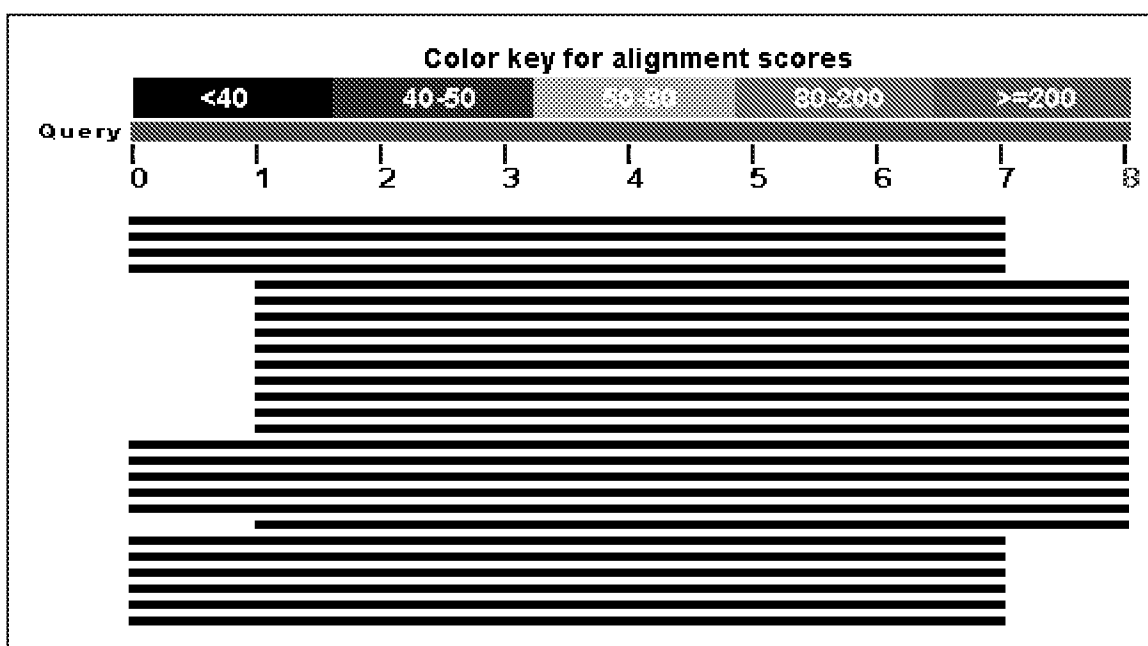
No putative conserved domains have been detected



## Distribution of 101 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





## Descriptions

		Score	
E		(Bits)	Value
Sequences producing significant alignments:			
emb CAA46601.1	urinary plasminogen activator [Rattus norvegi...	25.2	708
ref NP_037217.3	plasminogen activator, urokinase [Rattus nor...	25.2	708
sp P29598.1 UPOK_RAT	RecName: Full=Urokinase-type plasminogen...	25.2	708
ref NP_032899.1	plasminogen activator, urokinase [Mus muscul...	25.2	708
gb ACX36965.1	middle S protein [Hepatitis B virus] >gb ACX36...	24.8	949
gb ACX36957.1	middle S protein [Hepatitis B virus]	24.8	949
gb AEU97123.1	S protein [Hepatitis B virus]	24.8	949
gb AEI17005.1	surface antigen [Hepatitis B virus]	24.8	949
gb BAG12008.1	S protein [Hepatitis B virus]	24.8	949
ref XP_001450163.1	hypothetical protein [Paramecium tetraure...	24.6	949
gb AAZ59509.1	HBsAg [Hepatitis B virus]	24.6	949
gb AAZ59315.1	HBsAg [Hepatitis B virus]	24.6	949
gb AAA61740.1	51C surface protein [Paramecium tetraurelia]	24.8	949
gb AAW65562.1	HBsAg [Hepatitis B virus]	24.8	949
gb AAD13661.1	surface antigen [Hepatitis B virus]	23.5	2294
gb ACB45647.1	truncated S protein [Hepatitis B virus]	23.1	3077
gb ACB45646.1	truncated large S protein [Hepatitis B virus]	23.1	3077
ref XP_001750707.1	hypothetical protein [Monosiga brevicolli...	23.1	3077
ref XP_002092075.1	GE11868 [Drosophila yakuba] >gb EDW91787....	22.7	4129
gb EFA75884.1	hypothetical protein PPL_10456 [Polysphondyliu...	22.3	5541
ref YP_003006388.1	Cof-like hydrolase [Dickeya zeae Ech1591]...	22.3	5541
gb EEE22595.1	BNR/Asp-box repeat domain-containing protein, ...	22.3	5541
ref XP_002368431.1	sortilin, putative [Toxoplasma gondii ME4...	22.3	5541
ref NP_001144615.1	hypothetical protein LOC100277631 [Zea ma...	22.3	5541
ref XP_001742225.1	hypothetical protein [Monosiga brevicolli...	22.3	5541
ref XP_001764053.1	predicted protein [Physcomitrella patens ...	22.3	5541
ref YP_001669438.1	FAD dependent oxidoreductase [Pseudomonas...	22.3	5541
ref XP_001756901.1	predicted protein [Physcomitrella patens ...	22.3	5541
ref XP_638862.1	hypothetical protein DDB_G0283853 [Dictyoste...	22.3	5541
ref XP_638860.1	hypothetical protein DDB_G0283869 [Dictyoste...	22.3	5541
ref XP_638863.1	hypothetical protein DDB_G0283787 [Dictyoste...	22.3	5541
gb EFA829915.1	hypothetical protein PANDA_005925 [Ailuropoda ...	21.8	7434
gb EFA82002.1	hypothetical protein PPL_05237 [Polysphondyliu...	21.8	7434
gb EFA82001.1	carbohydrate-binding domain-containing protein...	21.8	7434
ref ZP_06141814.1	pectinesterase [Ruminococcus flavefaciens ...	21.8	7434
emb CBH16504.1	periodic tryptophan protein 2, putative; pred...	21.8	7434
ref XP_002444714.1	hypothetical protein SORBIDRAFT_07g026515...	21.8	7434
ref XP_002578344.1	transcription initiation factor brf1 [Sch...	21.8	7434
ref YP_002756665.1	lipoprotein [Escherichia coli] >gb ACL520...	21.8	7434
ref YP_002731228.1	cytochrome C family protein [Persephonell...	21.8	7434
ref XP_001013897.2	hypothetical protein THERM_01486710 [Tet...	21.8	7434
ref ZP_03726320.1	DNA topoisomerase (ATP-hydrolyzing) [Opitu...	21.8	7434
gb EEE55720.1	hypothetical protein OsJ_04192 [Oryza sativa J...	21.8	7434
ref XP_002290185.1	predicted protein [Thalassiosira pseudona...	21.8	7434
ref YP_002418785.1	putative lipoprotein [Escherichia coli] >...	21.8	7434
ref XP_002412137.1	hypothetical protein IscW_ISCW011495 [Ixo...	21.8	7434
ref XP_002598165.1	hypothetical protein BRAFLDRAFT_123314 [B...	21.8	7434
ref XP_002612022.1	hypothetical protein BRAFLDRAFT_86993 [Br...	21.8	7434


ref XP_002613108.1	hypothetical protein BRAFLDRAFT_89993 [Br...	21.8	7434
ref XP_002124394.1	PREDICTED: similar to integrin beta Hr1 [...	21.8	7434
dbj BAG65498.1	unnamed protein product [Homo sapiens]	21.8	7434
gb AAI66315.1	LOC100158602 protein [Xenopus (Silurana) tropi...	21.8	7434
ref XP_001912476.1	unnamed protein product [Podospira anseri...	21.8	7434
ref XP_001907985.1	unnamed protein product [Podospira anseri...	21.8	7434
ref XP_001770300.1	predicted protein [Physcomitrella patens ...	21.8	7434
ref XP_001775575.1	p300/CBP acetyltransferase-related protei...	21.8	7434
ref XP_001785357.1	p300/CBP acetyltransferase-related protei...	21.8	7434
ref ZP_02094454.1	hypothetical protein PEPMIC_01220 [Parvimo...	21.8	7434
ref XP_963736.2	hypothetical protein NCU03244 [Neurospora cr...	21.8	7434
ref XP_001502309.1	PREDICTED: fibrillin 1 [Equus caballus]	21.8	7434
ref ZP_01894398.1	hypothetical protein MDG893_13589 [Marinob...	21.8	7434
gb EDL80069.1	fibrillin 1, isoform CRA_a [Rattus norvegicus]...	21.8	7434
gb EDL80071.1	fibrillin 1, isoform CRA_b [Rattus norvegicus]	21.8	7434
gb EDL28139.1	fibrillin 1, isoform CRA_a [Mus musculus] >gb ...	21.8	7434
ref XP_001393188.1	hypothetical protein An08g10840 [Aspergil...	21.8	7434
ref XP_001369848.1	PREDICTED: hypothetical protein [Monodelp...	21.8	7434
gb EAY76601.1	hypothetical protein OsI_04550 [Oryza sativa I...	21.8	7434
ref XP_001443583.1	hypothetical protein [Paramecium tetraure...	21.8	7434
ref ZP_01693530.1	conserved protein [Microscilla marina ATCC...	21.8	7434
gb EAW77353.1	fibrillin 1 (Marfan syndrome), isoform CRA_a [...	21.8	7434
ref NP_000129.3	fibrillin 1 precursor [Homo sapiens] >sp P35...	21.8	7434
ref NP_032019.2	fibrillin 1 [Mus musculus] >emb CAM22806.1  ...	21.8	7434
ref XP_856076.1	drug/metabolite exporter family transporter ...	21.8	7434
ref XP_001149266.1	PREDICTED: fibrillin 1 [Pan troglodytes]	21.8	7434
ref NP_001044899.1	Os01g0865600 [Oryza sativa (japonica cult...	21.8	7434
ref XP_397600.3	PREDICTED: similar to family with sequence s...	21.8	7434
ref XP_392100.3	PREDICTED: similar to CG16791-PA [Apis melli...	21.8	7434
ref XP_001100608.1	PREDICTED: estrogen-related receptor beta...	21.8	7434
ref XP_001113107.1	PREDICTED: similar to fibrillin 1 precurs...	21.8	7434
ref ZP_01306957.1	hypothetical protein RED65_16411 [Oceanoba...	21.8	7434
ref XP_861706.1	PREDICTED: similar to Fibrillin-1 precursor ...	21.8	7434
ref XP_535468.2	PREDICTED: similar to Fibrillin-1 precursor ...	21.8	7434
dbj EAD92077.1	fibrillin 1 variant [Homo sapiens]	21.8	7434
dbj EAD81907.1	bHLH transcription factor-like protein [Oryza...	21.8	7434
gb AAT94187.1	PilL [Escherichia coli]	21.8	7434
ref YP_308679.1	lipoprotein [Escherichia coli] >gb AAL18827....	21.8	7434
gb AAL05516.1	AF399919_3 PilL [Escherichia coli]	21.8	7434
emb CAD19195.1	novel protein similar to MHC class II beta ch...	21.8	7434
ref XP_001030843.1	hypothetical protein THERM_01006510 [Tet...	21.8	7434
gb AAC62317.1	mutant fibrillin-1 [Mus musculus]	21.8	7434
gb AAA64217.1	fibrillin-1 [Mus musculus]	21.8	7434
ref XP_861733.1	PREDICTED: similar to Fibrillin-1 precursor ...	21.8	7434
ref XP_861765.1	PREDICTED: similar to Fibrillin-1 precursor ...	21.8	7434
ref XP_861792.1	PREDICTED: similar to Fibrillin-1 precursor ...	21.8	7434
ref NP_114013.1	fibrillin 1 [Rattus norvegicus] >gb AAD34438...	21.8	7434
dbj EAD16739.1	fibrillin 1 [Homo sapiens]	21.8	7434
ref XP_002633929.1	C. briggsae CBR-LAM-1 protein [Caenorhabd...	21.8	7434

```

ref|NP_001001771.1| fibrillin 1 precursor [Sus scrofa] >sp|Q9... 21.8 7434
prf||1713408A fibrillin 21.8 7434
sp|Q61554.1|FBN1_MOUSE RecName: Full=Fibrillin-1; Flags: Prec... 21.8 7434

```

Alignments [Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) [NEW](#)

>emb|CAA46601.1|  urinary plasminogen activator [Rattus norvegicus]  
Length=432




**GENE ID: 25619 Plau** | plasminogen activator, urokinase [Rattus norvegicus]  
(Over 10 PubMed links)

Score = 25.2 bits (52), Expect = 708  
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

```

Query 1 RTSTGQC 7
      RTSTGQC
Sbjct 283 RTSTGQC 289

```

>ref|NP\_037217.3|  plasminogen activator, urokinase [Rattus norvegicus]  
gb|AAI05860.1|  Plasminogen activator, urokinase [Rattus norvegicus]  
gb|EDL86256.1|  rCG41849 [Rattus norvegicus]  
Length=432



**GENE ID: 25619 Plau** | plasminogen activator, urokinase [Rattus norvegicus]  
(Over 10 PubMed links)

Score = 25.2 bits (52), Expect = 708  
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

```

Query 1 RTSTGQC 7
      RTSTGQC
Sbjct 283 RTSTGQC 289

```

>sp|P29598.1|UROK\_RAT  RecName: Full=Urokinase-type plasminogen activator; Short=U-plasminogen activator; Contains: RecName: Full=Urokinase-type plasminogen activator long chain A; Contains: RecName: Full=Urokinase-type plasminogen activator short chain A; Contains: RecName: Full=Urokinase-type plasminogen activator chain B; Flags: Precursor  
emb|CAA45028.1|  urikine-type plasminogen activator [Rattus norvegicus]  
Length=432






**GENE ID: 25619 Plau** | plasminogen activator, urokinase [Rattus norvegicus]  
(Over 10 PubMed links)



Score = 25.2 bits (52), Expect = 708  
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

```

Query 1 RTSTGQC 7
      RTSTGQC
Sbjct 283 RTSTGQC 289

```

>ref|NP\_032899.1|  plasminogen activator, urokinase [Mus musculus]  
sp|P06869.1|UROK\_MOUSE  RecName: Full=Urokinase-type plasminogen activator; Short=uPA; Contains: RecName: Full=Urokinase-type plasminogen activator long chain A; Contains: RecName: Full=Urokinase-type plasminogen activator short chain A; Contains: RecName: Full=Urokinase-type plasminogen activator chain B; Flags: Precursor  
emb|CAA26231.1|  unnamed protein product [Mus musculus]  
gb|AAA40539.1|  urokinase-type plasminogen activator [Mus musculus]  
gb|AAI20710.1|  Plasminogen activator, urokinase [Mus musculus]

**gb|AAI20714.1|**  Plasminogen activator, urokinase [Mus musculus]  
**gb|EDL01484.1|**  plasminogen activator, urokinase [Mus musculus]  
**dbj|BAH02680.1|** urokinase-type plasminogen activator [Mammalian expression vect  
 pmAlbEPintPlauGH]  
 Length=433

**GENE ID: 18792 Plau** | plasminogen activator, urokinase [Mus musculus]  
 (Over 100 PubMed links)

Score = 25.2 bits (52), Expect = 708  
 Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 RTSTGQC 7  
 RTSTGQC  
 Sbjct 284 RTSTGQC 290

>**gb|ACX36965.1|** middle S protein [Hepatitis B virus]  
**gb|ACX36975.1|** middle S protein [Hepatitis B virus]  
 Length=243

Score = 24.8 bits (51), Expect = 949  
 Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8  
 TSTGQCK  
 Sbjct 133 TSTGQCK 139

>**gb|ACX36957.1|** middle S protein [Hepatitis B virus]  
 Length=243

Score = 24.8 bits (51), Expect = 949  
 Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8  
 TSTGQCK  
 Sbjct 133 TSTGQCK 139

>**gb|ABU97123.1|** S protein [Hepatitis B virus]  
 Length=57

Score = 24.8 bits (51), Expect = 949  
 Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8  
 TSTGQCK  
 Sbjct 9 TSTGQCK 15

>**gb|ABI17005.1|** surface antigen [Hepatitis B virus]  
 Length=57



Score = 24.8 bits (51), Expect = 949  
 Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8  
 TSTGQCK  
 Sbjct 9 TSTGQCK 15

>**dbj|BAG12008.1|** S protein [Hepatitis B virus]  
 Length=254

Score = 24.8 bits (51), Expect = 949  
 Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8  
 TSTGQCK  
 Sbjct 144 TSTGQCK 150

>**ref|XP\_001450163.1|**  hypothetical protein [Paramecium tetraurelia strain d4-  
**emb|CAK82766.1|**  unnamed protein product [Paramecium tetraurelia]  
 Length=2233

**GENE ID: 5035948 GSPATT00017138001** | hypothetical protein  
[Paramecium tetraurelia strain d4-2]

Score = 24.8 bits (51), Expect = 949  
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8  
TSTGQCK  
Sbjct 1936 TSTGQCK 1942

>**gb|AA59509.1|** HBsAg [Hepatitis B virus]  
Length=101

Score = 24.8 bits (51), Expect = 949  
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8  
TSTGQCK  
Sbjct 5 TSTGQCK 11

>**gb|AA59315.1|** HBsAg [Hepatitis B virus]  
Length=101

Score = 24.8 bits (51), Expect = 949  
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8  
TSTGQCK  
Sbjct 5 TSTGQCK 11

>**gb|AA61740.1|** 51C surface protein [Paramecium tetraurelia]  
Length=2233

Score = 24.8 bits (51), Expect = 949  
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8  
TSTGQCK  
Sbjct 1936 TSTGQCK 1942

>**gb|AA65562.1|** HBsAg [Hepatitis B virus]  
Length=226

Score = 24.8 bits (51), Expect = 949  
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8  
TSTGQCK  
Sbjct 116 TSTGQCK 122

>**gb|AAD13661.1|** surface antigen [Hepatitis B virus]  
Length=226

Score = 23.5 bits (48), Expect = 2294  
Identities = 7/8 (87%), Positives = 7/8 (87%), Gaps = 0/8 (0%)

Query 1 RTSTGQCK 8  
RTSTG CK  
Sbjct 115 RTSTGPCK 122

>**gb|ACB45647.1|** truncated S protein [Hepatitis B virus]  
Length=171



Score = 23.1 bits (47), Expect = 3077  
Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query 1 RTST---GQCK 8  
RTST GQCK  
Sbjct 112 RTSTTGQCK 122

>**gb|ACB45646.1|** truncated large S protein [Hepatitis B virus]  
Length=345

Score = 23.1 bits (47), Expect = 3077  
Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)



Query 1 RTST---GQCK 8  
RTST GQCK  
Sbjct 286 RTSTTGQCK 296

>ref|XP\_001750707.1|  hypothetical protein [Monosiga brevicollis MX1]  
gb|EDQ84520.1|  predicted protein [Monosiga brevicollis MX1]  
Length=1216

GENE ID: 5895935 MONBRDRAFT\_30197 | hypothetical protein  
[Monosiga brevicollis MX1]

Score = 23.1 bits (47), Expect = 3077  
Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query 1 RTSTGQ---CK 8  
RTSTGQ CK  
Sbjct 451 RTSTGQVIACK 461

>ref|XP\_002092075.1|  GE11868 [Drosophila yakuba]  
gb|EDW91787.1|  GE11868 [Drosophila yakuba]  
Length=817

GENE ID: 6531266 Dyak\GE11868 | GE11868 gene product from transcript GE11868-RA  
[Drosophila yakuba] (10 or fewer PubMed links)

Score = 22.7 bits (46), Expect = 4129  
Identities = 7/8 (87%), Positives = 7/8 (87%), Gaps = 0/8 (0%)

Query 1 RTSTGQCK 8  
RTSTGQ K  
Sbjct 389 RTSTGQSK 396



>gb|EFA75884.1| hypothetical protein PPL\_10456 [Polysphondylium pallidum PN500]  
Length=641

Score = 22.3 bits (45), Expect = 5541  
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8  
T+TGQCK  
Sbjct 242 TATGQCK 248

Score = 19.7 bits (39), Expect = 32333  
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8  
TS GQCK  
Sbjct 158 TSDGQCK 164

>ref|YP\_003006388.1|  Cof-like hydrolase [Dickeya zeae Ech1591]  
gb|ACT08909.1|  Cof-like hydrolase [Dickeya zeae Ech1591]  
Length=279

GENE ID: 8120965 Dd1591\_4113 | Cof-like hydrolase [Dickeya zeae Ech1591]

Score = 22.3 bits (45), Expect = 5541  
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)


Query 1 RTSTGQC 7  
RTSTG+C  
Sbjct 84 RTSTGEC 90


>gb|EEE22595.1| BNR/Asp-box repeat domain-containing protein, putative [Toxoplasma gondii GT1]  
gb|EEE31368.1| BNR/Asp-box repeat domain-containing protein, putative [Toxoplasma gondii VEG]

Length=962

Score = 22.3 bits (45), Expect = 5541  
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 RTSTGQC 7  
RTSTG+C  
Sbjct 374 RTSTGEC 380


>ref|XP\_002368431.1|  sortilin, putative [Toxoplasma gondii ME49]


gb|EEB01291.1|  sortilin, putative [Toxoplasma gondii ME49]  
Length=962

**GENE ID: 7897795 TGME49\_090160** | sortilin, putative [Toxoplasma gondii ME49]

Score = 22.3 bits (45), Expect = 5541  
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 RTSTGQC 7  
RTSTG+C  
Sbjct 374 RTSTGEC 380


>ref|NP\_001144615.1|  hypothetical protein LOC100277631 [Zea mays]


gb|ACG41806.1|  hypothetical protein [Zea mays]  
Length=496

**GENE ID: 100277631 LOC100277631** | hypothetical protein LOC100277631 [Zea mays]  
(10 or fewer PubMed links)

Score = 22.3 bits (45), Expect = 5541  
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 RTSTGQC 7  
RTSTG+C  
Sbjct 189 RTSTGEC 195


>ref|XP\_001742225.1|  hypothetical protein [Monosiga brevicollis MX1]


gb|EDQ92463.1|  predicted protein [Monosiga brevicollis MX1]  
Length=1201

**GENE ID: 5887979 MONBRDRAFT\_22150** | hypothetical protein  
[Monosiga brevicollis MX1]

Score = 22.3 bits (45), Expect = 5541  
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 RTSTGQC 7  
RTSTG+C  
Sbjct 41 RTSTGEC 47


>ref|XP\_001764053.1|  predicted protein [Physcomitrella patens subsp. patens]


gb|EDQ71192.1|  predicted protein [Physcomitrella patens subsp. patens]  
Length=374

**GENE ID: 5927198 PHYPADRAFT\_77455** | hypothetical protein  
[Physcomitrella patens subsp. patens] (10 or fewer PubMed links)

Score = 22.3 bits (45), Expect = 5541  
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 RTSTGQC 7  
RTS+GQC  
Sbjct 189 RTSSGQC 195




>ref|YP\_001669438.1|  FAD dependent oxidoreductase [Pseudomonas putida GB-1]

gb|ABY99102.1|  FAD dependent oxidoreductase [Pseudomonas putida GB-1]  
Length=378

**GENE ID: 5870995 PputGB1\_3210** | FAD dependent oxidoreductase  
[Pseudomonas putida GB-1]

Score = 22.3 bits (45), Expect = 5541  
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)



Query 1 RTSTGQC 7  
RTS+GQC  
Sbjct 186 RTSSGQC 192

>ref|XP\_001756901.1|  predicted protein [Physcomitrella patens subsp. patens]  
dbj|BAB39467.1|  putative alpha-glucosidase [Physcomitrella patens subsp. pate  
gb|EDQ78132.1|  predicted protein [Physcomitrella patens subsp. patens]  
Length=916

**GENE ID: 5920253 PHYPADRAFT\_205099** | hypothetical protein  
[Physcomitrella patens subsp. patens] (10 or fewer PubMed links)

Score = 22.3 bits (45), Expect = 5541  
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)



Query 1 RTSTGQC 7  
RTSTG+C  
Sbjct 146 RTSTGEC 152

>ref|XP\_638862.1|  hypothetical protein DDB\_G0283853 [Dictyostelium discoideum]  
gb|EAL65541.1|  hypothetical protein DDB\_G0283853 [Dictyostelium discoideum AX  
Length=628

**GENE ID: 8624260 DDB\_G0283853** | hypothetical protein  
[Dictyostelium discoideum AX4] (10 or fewer PubMed links)

Score = 22.3 bits (45), Expect = 5541  
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)



Query 2 TSTGQCK 8  
T+TGQCK  
Sbjct 287 TNTGQCK 293

>ref|XP\_638860.1|  hypothetical protein DDB\_G0283869 [Dictyostelium discoideum]  
gb|EAL65549.1|  hypothetical protein DDB\_G0283869 [Dictyostelium discoideum AX  
Length=1141

**GENE ID: 8624258 DDB\_G0283869** | hypothetical protein  
[Dictyostelium discoideum AX4] (10 or fewer PubMed links)

Score = 22.3 bits (45), Expect = 5541  
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8  
T+TGQCK  
Sbjct 798 TNTGQCK 804

>ref|XP\_638863.1|  hypothetical protein DDB\_G0283787 [Dictyostelium discoideu  
gb|EAL65508.1|  hypothetical protein DDB\_G0283787 [Dictyostelium discoideum AX  
Length=1064

**GENE ID: 8624261 DDB\_G0283787** | hypothetical protein  
[Dictyostelium discoideum AX4] (10 or fewer PubMed links)

Score = 22.3 bits (45), Expect = 5541  
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8  
T+TGQCK  
Sbjct 728 TNTGQCK 734

>gb|EFB29915.1| hypothetical protein PANDA 005925 [Ailuropoda melanoleuca]

Length=2869

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC  
Sbjct 1842 TSTGQC 1847

>**gb|EFA82002.1|** hypothetical protein PPL\_05237 [Polysphondylium pallidum PN500]  
Length=1715

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8  
TSTG+CK  
Sbjct 990 TSTGECK 996

>**gb|EFA82001.1|** carbohydrate-binding domain-containing protein [Polysphondylium pallidum PN500]  
Length=705

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8  
TSTG+CK  
Sbjct 527 TSTGECK 533

>**ref|ZP\_06141814.1|** pectinesterase [Ruminococcus flavefaciens FD-1]  
Length=374



Score = 21.8 bits (44), Expect = 7434  
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 1 RTSTGQC 7  
RT IGQC  
Sbjct 27 RTGTGQC 33

>**emb|CBH16504.1|** periodic tryptophan protein 2, putative; predicted WD40 repeat protein [Trypanosoma brucei gambiense DAL972]  
Length=939

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)



Query 1 RTSTGQC 7  
R STGQC  
Sbjct 432 RASTGQC 438

>**ref|XP\_002444714.1|**  hypothetical protein SORBIDRAFT\_07g026515 [Sorghum bicolor]  
**gb|EES14209.1|**  hypothetical protein SORBIDRAFT\_07g026515 [Sorghum bicolor]  
Length=394

**GENE ID: 8060966 SORBIDRAFT\_07g026515** | hypothetical protein [Sorghum bicolor]  
(10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC  
Sbjct 150 TSTGQC 155


>**ref|XP\_002578344.1|**  transcription initiation factor brf1 [Schistosoma mansoni]  
**emb|CAZ34582.1|**  transcription initiation factor brf1, putative [Schistosoma manson]  
Length=770

**GENE ID: 8348817 Smp\_071570** | transcription initiation factor brf1  
[Schistosoma mansoni] (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC  
Sbjct 43 TSTGQC 48


>ref|YP\_002756665.1|  lipoprotein [Escherichia coli]


gb|ACL52052.1|  lipoprotein [Escherichia coli]  
Length=356

**GENE ID: 7701488 p026VIR\_p114** | lipoprotein [Escherichia coli]

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 1 RTSTGQC 7  
RTST QC  
Sbjct 340 RTSTAQC 346

>ref|YP\_002731228.1|  cytochrome C family protein [Persephonella marina EX-H1]


gb|ACO04288.1|  cytochrome C family protein [Persephonella marina EX-H1]  
Length=326

**GENE ID: 7675008 PERMA\_1460** | cytochrome C family protein  
[Persephonella marina EX-H1] (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC  
Sbjct 226 TSTGQC 231

>ref|XP\_001013897.2|  hypothetical protein TTHERM\_01486710 [Tetrahymena thermop]

gb|EAR93652.2|  hypothetical protein TTHERM\_01486710 [Tetrahymena thermophila  
SB210]  
Length=2346

**GENE ID: 7823083 TTHERM\_01486710** | hypothetical protein  
[Tetrahymena thermophila]

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC  
Sbjct 769 TSTGQC 774

>ref|ZP\_03726320.1| DNA topoisomerase (ATP-hydrolyzing) [Opitutaceae bacterium T  
gb|EEG19652.1| DNA topoisomerase (ATP-hydrolyzing) [Opitutaceae bacterium TAV2]  
Length=788



Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC  
Sbjct 493 TSTGQC 498

>gb|EEE55720.1| hypothetical protein OsJ\_04192 [Oryza sativa Japonica Group]  
Length=904

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)



Query 3 STGQCK 8  
STGQCK  
Sbjct 676 STGQCK 681

>ref|XP\_002290185.1|  predicted protein [Thalassiosira pseudonana CCMP1335]  
 gb|EED91937.1|  predicted protein [Thalassiosira pseudonana CCMP1335]  
 Length=2183

**GENE ID: 7449574 THAPSDRAFT\_22658** | hypothetical protein  
 [Thalassiosira pseudonana CCMP1335] (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434  
 Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)



Query 2 TSTGQC 7  
 TSTGQC  
 Sbjct 1235 TSTGQC 1240

>ref|YP\_002418785.1|  putative lipoprotein [Escherichia coli]  
 emb|CAQ87359.1|  putative lipoprotein [Escherichia coli]  
 Length=355

**GENE ID: 7872117 pill** | putative lipoprotein [Escherichia coli ED1a]

Score = 21.8 bits (44), Expect = 7434  
 Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)



Query 1 RTSTGQC 7  
 RTST QC  
 Sbjct 339 RTSTAQC 345

>ref|XP\_002412137.1|  hypothetical protein IscW\_ISCW011495 [Ixodes scapularis]  
 gb|EEC14721.1|  hypothetical protein IscW\_ISCW011495 [Ixodes scapularis]  
 Length=103

**GENE ID: 8036937 IscW\_ISCW011495** | hypothetical protein [Ixodes scapularis]

Score = 21.8 bits (44), Expect = 7434  
 Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)



Query 3 STGQCK 8  
 STGQCK  
 Sbjct 37 STGQCK 42

>ref|XP\_002598165.1|  hypothetical protein BRAFLDRAFT\_123314 [Branchiostoma flo  
 gb|EEN54177.1|  hypothetical protein BRAFLDRAFT\_123314 [Branchiostoma floridae]  
 Length=700

**GENE ID: 7231595 BRAFLDRAFT\_123314** | hypothetical protein  
 [Branchiostoma floridae] (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434  
 Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)



Query 3 STGQCK 8  
 STGQCK  
 Sbjct 608 STGQCK 613

>ref|XP\_002612022.1|  hypothetical protein BRAFLDRAFT\_86993 [Branchiostoma fl  
 gb|EEN68031.1|  hypothetical protein BRAFLDRAFT\_86993 [Branchiostoma floridae]  
 Length=1268

**GENE ID: 7243150 BRAFLDRAFT\_86993** | hypothetical protein  
 [Branchiostoma floridae] (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434  
 Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)


Query 2 TSTGQC 7  
 TSTGQC  
 Sbjct 270 TSTGQC 275

>ref|XP\_002613108.1|  hypothetical protein BRAFLDRAFT\_89993 [Branchiostoma fl  
gb|EEN69117.1|  hypothetical protein BRAFLDRAFT\_89993 [Branchiostoma floridae]  
Length=219

**GENE ID: 7209147 BRAFLDRAFT\_89993** | hypothetical protein  
[Branchiostoma floridae] (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/8 (75%), Positives = 7/8 (87%), Gaps = 0/8 (0%)


Query 1 RTSTGQCK 8  
RT +GQCK  
Sbjct 36 RTGSGQCK 43

>ref|XP\_002124394.1|  PREDICTED: similar to integrin beta Hr1 [Ciona intestinal  
Length=840

**GENE ID: 100180214 LOC100180214** | similar to integrin beta Hr1  
[Ciona intestinalis]

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)


Query 3 STGQCK 8  
STGQCK  
Sbjct 731 STGQCK 736

>dbj|BAG65498.1|  unnamed protein product [Homo sapiens]  
Length=1149

**GENE ID: 2200 FBN1** | fibrillin 1 [Homo sapiens] (Over 100 PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)


Query 2 TSTGQC 7  
TSTGQC  
Sbjct 732 TSTGQC 737


>gb|AAI66315.1|  LOC100158602 protein [Xenopus (Silurana) tropicalis]  
Length=883

**GENE ID: 100158602 LOC100158602** | hypothetical protein LOC100158602  
[Xenopus (Silurana) tropicalis] (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 3 STGQCK 8  
STGQCK  
Sbjct 793 STGQCK 798


>ref|XP\_001912476.1|  unnamed protein product [Podospira anserina]


emb|CAP59957.1|  unnamed protein product [Podospira anserina]  
Length=588

**GENE ID: 6197588 PODANSg09524** | hypothetical protein  
[Podospira anserina DSM 980]

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC  
Sbjct 388 TSTGQC 393



>ref|XP\_001907985.1|  unnamed protein product [Podospira anserina]

**emb|CAP68658.1|**  unnamed protein product [Podospora anserina]  
Length=111

**GENE ID: 6192331 PODANSg5020** | hypothetical protein  
[Podospora anserina DSM 980]

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/8 (75%), Positives = 6/8 (75%), Gaps = 0/8 (0%)



Query 1 RTSTGQCK 8  
RTST CK  
Sbjct 60 RTSTSHCK 67

>**ref|XP\_001770300.1|**  predicted protein [Physcomitrella patens subsp. patens]  
**gb|EDQ64975.1|**  predicted protein [Physcomitrella patens subsp. patens]  
Length=559

**GENE ID: 5933481 PHYPADRAFT\_84461** | hypothetical protein  
[Physcomitrella patens subsp. patens] (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)



Query 3 STGQCK 8  
STGQCK  
Sbjct 304 STGQCK 309

>**ref|XP\_001775575.1|**  p300/CBP acetyltransferase-related protein [Physcomitre subsp. patens]  
**gb|EDQ59658.1|**  p300/CBP acetyltransferase-related protein [Physcomitrella pat subsp. patens]  
Length=1617

**GENE ID: 5938778 HAC1501** | p300/CBP acetyltransferase-related protein  
[Physcomitrella patens subsp. patens] (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8  
TSTG+CK  
Sbjct 1232 TSTGECK 1238

>**ref|XP\_001785357.1|**  p300/CBP acetyltransferase-related protein [Physcomitre subsp. patens]  
**gb|EDQ49842.1|**  p300/CBP acetyltransferase-related protein [Physcomitrella pat subsp. patens]  
Length=1082

**GENE ID: 5948557 HAC1502** | p300/CBP acetyltransferase-related protein  
[Physcomitrella patens subsp. patens] (10 or fewer PubMed links)



Score = 21.8 bits (44), Expect = 7434  
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 TSTGQCK 8  
TSTG+CK  
Sbjct 697 TSTGECK 703

>**ref|ZP\_02094454.1|** hypothetical protein PEPMIC\_01220 [Parvimonas micra ATCC 332  
**gb|EDP23416.1|** hypothetical protein PEPMIC\_01220 [Parvimonas micra ATCC 33270]  
Length=324

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 3 STGQCK 8  
STGQCK  
Sbjct 93 STGQCK 98

>ref|XP\_963736.2|  hypothetical protein NCU03244 [Neurospora crassa OR74A]  
gb|EAA34500.2|  conserved hypothetical protein [Neurospora crassa OR74A]  
Length=531

GENE ID: 3879885 NCU03244 | hypothetical protein [Neurospora crassa OR74A]  
(10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC  
Sbjct 343 TSTGQC 348

>ref|XP\_001502309.1|  PREDICTED: fibrillin 1 [Equus caballus]  
Length=2871

GENE ID: 100055741 FBN1 | fibrillin 1 [Equus caballus]



Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC  
Sbjct 1842 TSTGQC 1847

>ref|ZP\_01894398.1| hypothetical protein MDG893\_13589 [Marinobacter algicola DG8]  
gb|EDM47477.1| hypothetical protein MDG893\_13589 [Marinobacter algicola DG893]  
Length=137

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)


Query 2 TSTGQC 7  
TSTGQC  
Sbjct 116 TSTGQC 121

>gb|EDL80069.1|  fibrillin 1, isoform CRA\_a [Rattus norvegicus]  
gb|EDL80070.1|  fibrillin 1, isoform CRA\_a [Rattus norvegicus]  
Length=2872

GENE ID: 83727 Fbn1 | fibrillin 1 [Rattus norvegicus]  
(10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)



Query 2 TSTGQC 7  
TSTGQC  
Sbjct 1843 TSTGQC 1848

>gb|EDL80071.1|  fibrillin 1, isoform CRA\_b [Rattus norvegicus]  
Length=2807

GENE ID: 83727 Fbn1 | fibrillin 1 [Rattus norvegicus]  
(10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)



Query 2 TSTGQC 7  
TSTGQC  
Sbjct 1778 TSTGQC 1783

>gb|EDL28139.1|  fibrillin 1, isoform CRA\_a [Mus musculus]  
gb|EDL28140.1|  fibrillin 1, isoform CRA\_b [Mus musculus]  
Length=2873

GENE ID: 14118 Fbn1 | fibrillin 1 [Mus musculus] (Over 100 PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)


Query 2 TSTGQC 7  
TSTGQC  
Sbjct 1844 TSTGQC 1849

>ref|XP\_001393188.1|  hypothetical protein An08g10840 [Aspergillus niger]  
emb|CAK45757.1|  hypothetical protein [Aspergillus niger]  
Length=329

**GENE ID: 4983398 An08g10840** | hypothetical protein  
[Aspergillus niger CBS 513.88] (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC  
Sbjct 292 TSTGQC 297

>ref|XP\_001369848.1|  PREDICTED: hypothetical protein [Monodelphis domestica]  
Length=2871

**GENE ID: 100025769 LOC100025769** | hypothetical protein LOC100025769  
[Monodelphis domestica]



Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC  
Sbjct 1843 TSTGQC 1848

>gb|EAY76601.1| hypothetical protein OsI\_04550 [Oryza sativa Indica Group]  
Length=895

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 3 STGQCK 8  
STGQCK  
Sbjct 667 STGQCK 672

>ref|XP\_001443583.1|  hypothetical protein [Paramecium tetraurelia strain d4-  
emb|CAK76186.1|  unnamed protein product [Paramecium tetraurelia]  
Length=2350

**GENE ID: 5029368 GSPATT00011759001** | hypothetical protein  
[Paramecium tetraurelia strain d4-2]


Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC  
Sbjct 2043 TSTGQC 2048

>ref|ZP\_01693530.1| conserved protein [Microscilla marina ATCC 23134]  
gb|EAY25518.1| conserved protein [Microscilla marina ATCC 23134]  
Length=193

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)


Query 2 TSTGQC 7  
TSTGQC  
Sbjct 98 TSTGQC 103


>gb|EAW77353.1|  fibrillin 1 (Marfan syndrome), isoform CRA\_a [Homo sapiens]  
Length=2869


**GENE ID: 2200 FBN1** | fibrillin 1 [Homo sapiens] (Over 100 PubMed links)


Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC  
Sbjct 1842 TSTGQC 1847

>ref|NP\_000129.3|  fibrillin 1 precursor [Homo sapiens]

sp|P35555.2|FBN1\_HUMAN  RecName: Full=Fibrillin-1; Flags: Precursor

gb|EAW77354.1|  fibrillin 1 (Marfan syndrome), isoform CRA\_b [Homo sapiens]


gb|AAI46855.1|  Fibrillin 1 [Homo sapiens]

gb|ACZ58372.1| fibrillin 1 [Homo sapiens]  
Length=2871


**GENE ID: 2200 FBN1** | fibrillin 1 [Homo sapiens] (Over 100 PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC  
Sbjct 1842 TSTGQC 1847

>ref|NP\_032019.2|  fibrillin 1 [Mus musculus]


emb|CAM22806.1|  fibrillin 1 [Mus musculus]


emb|CAM17722.1|  fibrillin 1 [Mus musculus]  
Length=2873

**GENE ID: 14118 Fbn1** | fibrillin 1 [Mus musculus] (Over 100 PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC  
Sbjct 1844 TSTGQC 1849

>ref|YP\_856076.1|  drug/metabolite exporter family transporter [Aeromonas hydrophila subsp. hydrophila ATCC 7966]

gb|ABK39216.1|  transporter, 10 TMS drug/metabolite exporter (DME) family [Aeromonas hydrophila subsp. hydrophila ATCC 7966]  
Length=293

**GENE ID: 4487228 AHA\_1538** | drug/metabolite exporter family transporter [Aeromonas hydrophila subsp. hydrophila ATCC 7966] (10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 1 RTSTGQC 7  
R STGQC  
Sbjct 284 RASTGQC 290


>ref|XP\_001149266.1|  PREDICTED: fibrillin 1 [Pan troglodytes]  
Length=3004

**GENE ID: 453411 FBN1** | fibrillin 1 [Pan troglodytes]

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC


Sbjct 1975 TSTGQC 1980

>ref|NP\_001044899.1|  Os01g0865600 [Oryza sativa (japonica cultivar-group)]  
Length=921

**GENE ID: 4324795 Os01g0865600** | Os01g0865600 [Oryza sativa Japonica Group]  
(10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)


Query 3 STGQCK 8  
STGQCK  
Sbjct 693 STGQCK 698

>ref|XP\_397600.3|  PREDICTED: similar to family with sequence similarity 48,  
A isoform b [Apis mellifera]  
Length=1078

**GENE ID: 410031 LOC410031** | similar to family with sequence similarity 48,  
member A isoform b [Apis mellifera]

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)


Query 1 RTSTGQC 7  
R STGQC  
Sbjct 1005 RASTGQC 1011

>ref|XP\_392100.3|  PREDICTED: similar to CG16791-PA [Apis mellifera]  
Length=452

**GENE ID: 408555 LOC408555** | similar to CG16791-PA [Apis mellifera]  
(10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)


Query 2 TSTGQC 7  
TSTGQC  
Sbjct 419 TSTGQC 424

>ref|XP\_001100608.1|  PREDICTED: estrogen-related receptor beta isoform 2 [Ma  
Length=454

**GENE ID: 703799 ESRRB** | estrogen-related receptor beta [Macaca mulatta]

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC  
Sbjct 161 TSTGQC 166

>ref|XP\_001113107.1|  PREDICTED: similar to fibrillin 1 precursor [Macaca mul  
Length=2871

**GENE ID: 714451 LOC714451** | similar to fibrillin 1 precursor [Macaca mulatta]


Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC  
Sbjct 1842 TSTGQC 1847

>ref|ZP\_01306957.1| hypothetical protein RED65\_16411 [Oceanobacter sp. RED65]  
**gb|EAT12438.1|** hypothetical protein RED65\_16411 [Oceanobacter sp. RED65]  
Length=135

Score = 21.8 bits (44), Expect = 7434  
 Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)


Query 2 TSTGQC 7  
 TSTGQC  
 Sbjct 109 TSTGQC 114

>ref|XP\_861706.1|  PREDICTED: similar to Fibrillin-1 precursor isoform 3 [Canis familiaris]  
 Length=2417

**GENE ID: 478293 FBN1** | fibrillin 1 [Canis lupus familiaris]

Score = 21.8 bits (44), Expect = 7434  
 Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)


Query 2 TSTGQC 7  
 TSTGQC  
 Sbjct 1842 TSTGQC 1847

>ref|XP\_535468.2|  PREDICTED: similar to Fibrillin-1 precursor isoform 1 [Canis familiaris]  
 Length=2871

**GENE ID: 478293 FBN1** | fibrillin 1 [Canis lupus familiaris]

Score = 21.8 bits (44), Expect = 7434  
 Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
 TSTGQC  
 Sbjct 1842 TSTGQC 1847

>dbj|BAD92077.1|  fibrillin 1 variant [Homo sapiens]  
 Length=830

**GENE ID: 2200 FBN1** | fibrillin 1 [Homo sapiens] (Over 100 PubMed links)

Score = 21.8 bits (44), Expect = 7434  
 Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
 TSTGQC  
 Sbjct 277 TSTGQC 282

>dbj|BAD81907.1| bHLH transcription factor-like protein [Oryza sativa Japonica Group]

dbj|BAG90720.1| unnamed protein product [Oryza sativa Japonica Group]  
 dbj|BAF06813.2| Os01g0865600 [Oryza sativa Japonica Group]  
 Length=904



Score = 21.8 bits (44), Expect = 7434  
 Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 3 STGQCK 8  
 STGQCK  
 Sbjct 676 STGQCK 681

>gb|AAT94187.1| Pill [Escherichia coli]  
 Length=356

Score = 21.8 bits (44), Expect = 7434  
 Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 1 RTSTGQC 7  
 RTST QC  
 Sbjct 340 RTSTAQC 346

>ref|YP\_308679.1|  lipoprotein [Escherichia coli]  
 gb|AAL18827.2|  Lipoprotein [Escherichia coli]

Length=356

**GENE ID: 3654428 pill** | lipoprotein [Escherichia coli]  
(10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 1 RTSTGQC 7  
RTST QC  
Sbjct 340 RTSTAQC 346

>**gb|AAL05516.1|AF399919\_3** Pill [Escherichia coli]  
Length=357

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 1 RTSTGQC 7  
RTST QC  
Sbjct 341 RTSTAQC 347

>**emb|CAD19195.1|** novel protein similar to MHC class II beta chain [Danio rerio]  
Length=249

**GENE ID: 368615 si:busml-194e12.12** | si:busml-194e12.12 [Danio rerio]  
(10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 3 STGQCK 8  
STGQCK  
Sbjct 244 STGQCK 249

>**ref|XP\_001030843.1|** hypothetical protein TTHERM\_01006510 [Tetrahymena thermop  
**gb|EAR83180.1|** hypothetical protein TTHERM\_01006510 [Tetrahymena thermophila  
SB210]  
Length=1588

**GENE ID: 7842955 TTHERM\_01006510** | hypothetical protein  
[Tetrahymena thermophila]

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 3 STGQCK 8  
STGQCK  
Sbjct 287 STGQCK 292

>**gb|AAC62317.1|** mutant fibrillin-1 [Mus musculus]  
Length=3857

**GENE ID: 14118 Fbn1** | fibrillin 1 [Mus musculus] (Over 100 PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC  
Sbjct 2828 TSTGQC 2833


>**gb|AAA64217.1|** fibrillin-1 [Mus musculus]  
Length=2873

**GENE ID: 14118 Fbn1** | fibrillin 1 [Mus musculus] (Over 100 PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7


Sbjct 1844 TSTGQC 1849

>ref|XP\_861733.1|  PREDICTED: similar to Fibrillin-1 precursor isoform 4 [Canis familiaris]  
Length=2816

**GENE ID: 478293 FBN1** | fibrillin 1 [Canis lupus familiaris]

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)


Query 2 TSTGQC 7  
Sbjct 1842 TSTGQC 1847

>ref|XP\_861765.1|  PREDICTED: similar to Fibrillin-1 precursor isoform 5 [Canis familiaris]  
Length=2804

**GENE ID: 478293 FBN1** | fibrillin 1 [Canis lupus familiaris]

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)



Query 2 TSTGQC 7  
Sbjct 1787 TSTGQC 1792

>ref|XP\_861792.1|  PREDICTED: similar to Fibrillin-1 precursor isoform 6 [Canis familiaris]  
Length=2872

**GENE ID: 478293 FBN1** | fibrillin 1 [Canis lupus familiaris]

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)


Query 2 TSTGQC 7  
Sbjct 1843 TSTGQC 1848

>ref|NP\_114013.1|  fibrillin 1 [Rattus norvegicus]  
**gb|AAD34438.1|**  fibrillin-1 [Rattus norvegicus]  
Length=2872

**GENE ID: 83727 Fbn1** | fibrillin 1 [Rattus norvegicus]  
(10 or fewer PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
Sbjct 1843 TSTGQC 1848


>dbj|BAD16739.1|  fibrillin 1 [Homo sapiens]  
Length=2871

**GENE ID: 2200 FBN1** | fibrillin 1 [Homo sapiens] (Over 100 PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
Sbjct 1842 TSTGQC 1847


>ref|XP\_002633929.1|  C. briggsae CBR-LAM-1 protein [Caenorhabditis briggsae]

**emb|CAP37137.1|**  *C. briggsae* CBR-LAM-1 protein [Caenorhabditis briggsae]  
Length=1265


**GENE ID: 8575925 Cbr-lam-1** | *C. briggsae* CBR-LAM-1 protein  
[Caenorhabditis briggsae]

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 3 STGQCK 8  
STGQCK  
Sbjct 587 STGQCK 592

>**ref|NP\_001001771.1|**  fibrillin 1 precursor [Sus scrofa]

**sp|Q9TV36.1|FBN1\_PIG**  RecName: Full=Fibrillin-1; Flags: Precursor

**gb|AAD50328.1|AF073800\_1**  fibrillin-1 precursor [Sus scrofa]  
Length=2871

**GENE ID: 414836 FBN1** | fibrillin 1 [Sus scrofa] (10 or fewer PubMed links)


Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)


Query 2 TSTGQC 7  
TSTGQC  
Sbjct 1842 TSTGQC 1847

>**prf||1713408A** fibrillin  
Length=1973

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC  
Sbjct 944 TSTGQC 949

>**sp|Q61554.1|FBN1\_MOUSE**  RecName: Full=Fibrillin-1; Flags: Precursor

**gb|AAA56840.1|**  fibrillin [Mus musculus]  
Length=2871

**GENE ID: 14118 Fbn1** | fibrillin 1 [Mus musculus] (Over 100 PubMed links)

Score = 21.8 bits (44), Expect = 7434  
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

Query 2 TSTGQC 7  
TSTGQC  
Sbjct 1842 TSTGQC 1847

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